

# Mensural Discrimination of *Sorex longirostris* and *Sorex cinereus* (Insectivora: Soricidae) in the Southeastern United States

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**ABSTRACT**—The effectiveness of univariate and multivariate statistics in distinguishing *Sorex cinereus* and *S. longirostris* from the southeastern United States on the basis of standard body and cranial measurements was assessed. Eleven of 15 characters in univariate comparisons showed significant differences between species, but the range of measurements overlapped. Bivariate comparisons permit identification using external measurements, cranial and external measurements combined, and cranial measurements alone. Multivariate procedures permitted maximum distinction of the species. A discriminant function model is presented to permit identification on the basis of three cranial characters.

The masked shrew (*Sorex cinereus* Kerr 1792) is distributed throughout the transcontinental coniferous forests of North America from the Canadian Arctic south into the extreme northern portions of the United States with extension into the montane forests of the Rocky and Appalachian mountains (Hall 1981, Junge and Hoffmann 1981, van Zyll de Jong and Kirkland 1989, Laerm et al. 1995). The southeastern shrew (*Sorex longirostris* Bachman 1837) ranges from northern Missouri east through the southern portions of Illinois, Indiana, and Ohio to Maryland, and southward from eastern Oklahoma to Florida (French 1980a, 1980b; Hall 1981; Junge and Hoffmann 1981; and Jones et al. 1991). The two species have overlapping distributions in northcentral Missouri (Mock and Kivett 1980, Schwartz and Schwartz 1981, Greer 1989), southern Illinois (Hoffmeister 1989) and Indiana (Mumford and Whitaker 1982), and throughout much of the southern Appalachians from West Virginia and Virginia south to Georgia and South Carolina (Hall 1981, Pagels and Handley 1989, Jones et al. 1991, Ford et al. 1994, Laerm et al. 1995).

*Sorex cinereus* and *S. longirostris* are morphologically remarkably similar. The two are reported to differ in that *cinereus* is somewhat larger, has a longer tail (usually more than 31 mm), a comparatively longer and more slender rostrum, a higher braincase, and third unicuspid

larger than the fourth (French 1980a, Junge and Hoffman 1981, Jones et al. 1991). The latter character is frequently considered to be diagnostic (e.g., Hall 1981). However, numerous authors (Miller 1895; Jackson 1928; Kellogg 1939; French 1980a, 1980b, 1980c; Junge and Hoffmann 1981) point out that this is not always the case. French (1980a, 1980b) reported that 20% of *S. longirostris* examined in Alabama and Georgia and 12% of those in Indiana were characterized by third and fourth upper unicuspid that were equal or nearly equal in size. Similarly, some populations of *S. cinereus* exhibit third unicuspid that are smaller than the fourth. For example, Bole and Moulthrop (1942) described *S. c. ohioensis*, in part, on the basis of the third unicuspid being smaller than the fourth. Elsewhere, Kellogg (1939:251) suggested the synonymy of *S. fontinalis* (now regarded as a subspecies of *S. cinereus*; see van Zyll de Jong and Kirkland 1989) with *S. longirostris* concluding that "...the supposed distinctions between *S. longirostris* and *S. fontinalis* are nothing more than individual variation."

Qualitatively, *S. longirostris* and *S. cinereus* are not difficult to distinguish; as Jones et al. (1991:265) point out, "...under visual examination...skulls of the two species differed markedly, *S. longirostris* has a strongly arched palate and shorter rostrum, and the first two unicuspid are of larger diameter than the third and fourth. *S. cinereus* has a flat long palate and unicuspid of relatively uniform diameter." Unfortunately, qualitative comparisons are often frustratingly difficult to apply in the absence of a good comparative series. Jones et al. (1991) noted that *S. cinereus* and *S. longirostris* were so similar morphologically that they were not able to use *S. cinereus* as an out-group in their study of geographic variation of *S. longirostris*.

French (1980c) made quantitative comparisons between the two species using a univariate statistical analysis of cranial measurements of 162 *S. cinereus* and 110 *S. longirostris* from Virgo County, Indiana. He concluded that *S. cinereus* and *S. longirostris* were morphologically similar and that no single character was 100% diagnostic in distinguishing them. Although 13 standard body and cranial measurements differed significantly between *S. cinereus* and *S. longirostris*, none was characterized by non-overlapping ranges. Univariate morphological comparisons in Greer's (1989) study of seven cranial measurements indicated significant differences between the two species for six out of seven characters in Missouri; however, as in the French (1980c) study, there was considerable overlap.

We are not familiar with a published study of a multivariate morphometric comparison of the two species. The purpose of this paper is to examine the effectiveness of both univariate and multivariate

statistical procedures in distinguishing *S. cinereus* and *S. longirostris* from the southeastern United States, where the two species show a broad area of sympatry, on the basis of standard body and cranial measurements.

## MATERIALS AND METHODS

We used univariate and multivariate statistics to examine 200 museum specimens for morphological variation. To provide for robustness in our analysis and include any differences due to clinal variation, we selected 50 specimens of each species from the southern portion of its range in Georgia, North Carolina, and South Carolina and another 50 specimens from central and northern Virginia. *A priori* identifications were based on specimen tag information. In addition, we used six additional specimens of each species not used in the model building process to test the model. These were measured to the nearest 0.01 mm with dial calipers under a dissecting microscope. Specimens examined are listed in the Appendix.

Menzel measured the cranial characters to the nearest 0.01 mm with a Wild M400 Stereo microscope. Images were received by an Optronics VA-470 video camera and transferred to a 486 PC utilizing Analytical Imaging Concepts (Irvine, California) imaging software and stored in the TIF format. To assess the repeatability of the video measurement system, a set of 10 specimens were measured three times each. The set of 10 specimens was measured, then the order was randomized, and the set was measured again, and finally the order was again randomized and remeasured. Although video images could be stored for re-examination, each specimen was rescanned and the system was recalibrated prior to each remeasurement.

Eleven cranial characters (Table 1) were measured on all individuals: condylobasilar length (CBL), cranial breadth (CB), length of unicuspid toothrow (LUT), length of 1st unicuspid (LU1), breadth of 1st unicuspid (BU1), length of 3rd unicuspid (LU3), breadth of 3rd unicuspid (BU3), length of 4th unicuspid (LU4), breadth of 4th unicuspid (BU4), length of unicuspids 3 and 4 (LU34), and breadth across 2nd molars (BM2). External body measurements (total length, tail length, and hind foot length) and sex were recorded when available from specimen tags; body length was calculated by subtracting tail length from total length. Each specimen was assigned to one of 12 age classes based on the criteria of Rudd (1955).

Statistical analyses were performed with Systat 5.1a (Wilkinson 1989) and SPSS 4.01 (Norusis 1990). Univariate normality and homogeneity of variance were tested by inspection of plotted residuals and Bartlett's

Table 1. Mean, standard error (SE), and range of 14 measurements for northern (N) and southern (S) populations of *Sorex longirostris* and *S. cinereus*.

Character	<i>Sorex longirostris</i>			<i>Sorex cinereus</i>			
	Population	$\bar{x}$	SE	Range	$\bar{x}$	SE	Range
Total Length <sup>a</sup>	N	82.82	2.010	74-102	86.48	1.709	65-101
	S	75.42	0.842	67-86	86.00	0.598	76-93
Tail Length	N	30.41	0.875	25-34	36.61	0.443	34-41
	S	28.06	0.564	18-33	39.00	0.278	35-43
Hind-foot Length	N	10.56	0.250	9-13	11.17	0.149	10-13
	S	10.55	0.270	9-15	11.74	0.075	11-13
Body Length	N	52.41	1.364	44-64	49.87	1.533	29-64
	S	47.35	0.700	42-58	47.00	0.494	40-55
Condylbasilar Length (CBL) <sup>b</sup>	N	14.32	0.053	13.3-15.6	15.56	0.053	14.3-16.4
	S	14.57	0.045	13.9-15.4	15.85	0.049	14.8-16.7
Cranial Breadth (CB)	N	7.28	0.023	6.87-7.56	7.71	0.030	7.19-8.09
	S	7.31	0.030	6.64-7.78	7.75	0.031	7.26-8.20
Length of Unicuspid Toothrow	N	1.86	0.012	1.57-2.00	2.15	0.013	1.95-2.37
	S	1.87	0.011	1.63-2.04	2.22	0.014	1.88-2.44
Length of 1 <sup>st</sup> Unicuspid	N	0.41	0.004	0.32-0.46	0.48	0.005	0.40-0.55
	S	0.42	0.006	0.30-0.51	0.51	0.006	0.41-0.58
Breadth of 1 <sup>st</sup> Unicuspid	N	0.46	0.004	0.38-0.52	0.50	0.005	0.40-0.58
	S	0.46	0.005	0.38-0.56	0.51	0.007	0.40-0.61
Length of 3 <sup>rd</sup> Unicuspid	N	0.34	0.005	0.27-0.47	0.46	0.004	0.39-0.52
	S	0.34	0.005	0.25-0.47	0.47	0.005	0.39-0.56
Breadth of 3 <sup>rd</sup> Unicuspid	N	0.42	0.004	0.35-0.48	0.42	0.005	0.33-0.51
	S	0.43	0.005	0.37-0.53	0.42	0.005	0.31-0.52

Table 1. Continued.

Character	<i>Sorex longirostris</i>				<i>Sorex cinereus</i>			
	Population	$\bar{x}$	SE	Range	$\bar{x}$	SE	Range	
Length of 4 <sup>th</sup> Unicuspid	N	0.36	0.004	0.31-0.43	0.42	0.004	0.35-0.48	
	S	0.37	0.004	0.29-0.42	0.42	0.004	0.35-0.48	
Breadth of 4 <sup>th</sup> Unicuspid	N	0.42	0.004	0.36-0.49	0.43	0.005	0.35-0.50	
	S	0.43	0.006	0.34-0.51	0.42	0.005	0.33-0.50	
Length of Unicuspids 3 and 4	N	0.71	0.006	0.64-0.79	0.89	0.006	0.77-0.98	
	S	0.71	0.007	0.62-0.83	0.90	0.007	0.76-1.10	
Breadth Across 2nd Molars	N	3.72	0.016	3.43-3.91	3.52	0.014	3.29-3.72	
	S	3.84	0.021	3.56-4.27	3.64	0.015	3.31-3.84	

<sup>a</sup> Statistics for external characters were based on 17 and 31 for northern and southern *Sorex longirostris*, and 23 and 43 northern and southern *S. cinereus*, respectively.

<sup>b</sup> Statistics for cranial characters were based on sample size of approximately 50 in each group.

test for homogeneity of group variances, respectively. Inspection of residuals revealed that 12 of 2,400 measurements (200 specimens by 12 measurements) were found to be extreme ( $\geq 5$  standard deviations from the mean). Five of these extreme measurements were attributed to two individuals, and both individuals (USNM 75167, USNM 296566) were deleted from the analysis. The other extreme measurements were attributed to six different individuals. These six measurements and 11 other missing observations were replaced with the within-group mean of the character in question so that these individuals could be included in the multivariate analyses. After the extreme observations were corrected, we assumed multivariate normality based on marginal normality and multivariate homogeneity of variance based on failure of rejection in the test of equality of group covariance matrices using Box's M ( $P = 0.082$ ).

Differences among repeated measures, adult age classes, and sexes were tested with analysis of variance, and type-1 error rates were corrected with the sequential Bonferroni adjustment (Rice 1989) where necessary. Taxa were classified using stepwise discriminant analysis. Variables were included in the models based on minimizing Wilk's lambda, prior probabilities were equal to sample size, and varimax rotation was employed. Stepwise discriminant analysis will find an optimal solution based on the data; however, depending on which variables enter the model first, it may find a local optimum rather than the global optimum. To help avoid this optimization problem, we removed variables that entered the model in the first steps and repeated the analysis. All analyses were performed on raw data without transformation and without removing size (Rohlf and Bookstein 1987), because this produced the simplest tool for future classification of new specimens consistent with a goal of a high degree of group separation.

The model separating *S. cinereus* and *S. longirostris* was validated in two ways. First it was validated internally by randomly selecting subsets of the data (approximately 80% of the data selected without regard to species), constructing the discriminant model, and using that model to classify the remaining 20% of the specimens. This procedure was repeated 200 times. Second, because the skulls were originally measured utilizing a non-traditional approach, the model was validated externally with additional specimens (six test specimens of each species) measured with dial calipers under a dissecting microscope.

## RESULTS AND DISCUSSION

In the analysis of the repeated measures, no significant difference was found among measurements for any of the 11 cranial characters.

Very little of the total variance could be attributed to the repeated measures (range of 0 to 24%,  $\bar{x} = 5.5\%$ ), suggesting that with careful calibration the video system provided highly repeatable measurements.

In univariate comparisons of the sexes, only the length of unicuspid 3 and 4 (LU34) in *S. longirostris* differed significantly ( $P = 0.031$ ). Males and females averaged 0.71 mm (SE = 0.0064,  $n = 49$ ) and 0.69 mm (SE = 0.0091,  $n = 20$ ), respectively (Rice 1989). When this character was examined within regions, sexes did not differ significantly (southern sample,  $P = 0.23$ ; northern sample,  $P = 0.10$ ).

In a few cases, differences among age classes within species, regions, and sexes were individually, but not collectively, significant ( $\alpha \leq 0.05$ ). The only consistently significant ( $P < 0.01$ ) difference among age groups was length of first unicuspid (LU1) which tended to decrease in magnitude with increasing age.

In univariate analysis of morphological variation, all characters except body length, breadth of third unicuspid (BU3), and breadth of fourth unicuspid (BU4) differed significantly ( $P < 0.001$ ) between species. For all characters that showed significant differences, except breadth across second molars (BM2), *S. cinereus* was larger than *S. longirostris*. For character BM2, the size of *S. longirostris* exceeded *S. cinereus*. In all cases except tail length, however, the range of measurements for both species overlapped (Table 1).

Multivariate analysis using cranial measurements was successful in correctly identifying all specimens of the two species. However, the geographic origin of only 79% of the northern and southern specimens could be identified correctly. For *S. longirostris*, 11 southern and 11 northern specimens were incorrectly classified into the opposite geographic group; for *S. cinereus*, 7 southern and 12 northern specimens were incorrectly classified. Such a measure of geographic variation, perhaps clinal, was expected.

Discriminant analysis using cranial measurements for the two species correctly classified all specimens with three characters, LU34, BM2, and CBL, in order of inclusion into the model. Standardized canonical discriminant function coefficients were 0.60, 0.72, and -0.73 for LU34, BM2, and CBL, respectively. Pooled within-groups correlations between discriminating variables and canonical discriminant functions, variables ordered by size of correlation within function, were 0.69, -0.25, and 0.53 for these characters, respectively.

Unknown specimens can be identified to species with this latter model using unstandardized canonical discriminant function coefficients for the three variables. To do so, measure the unknown specimen for CBL, LU34, and BM2, then multiply each measurement by its coefficient

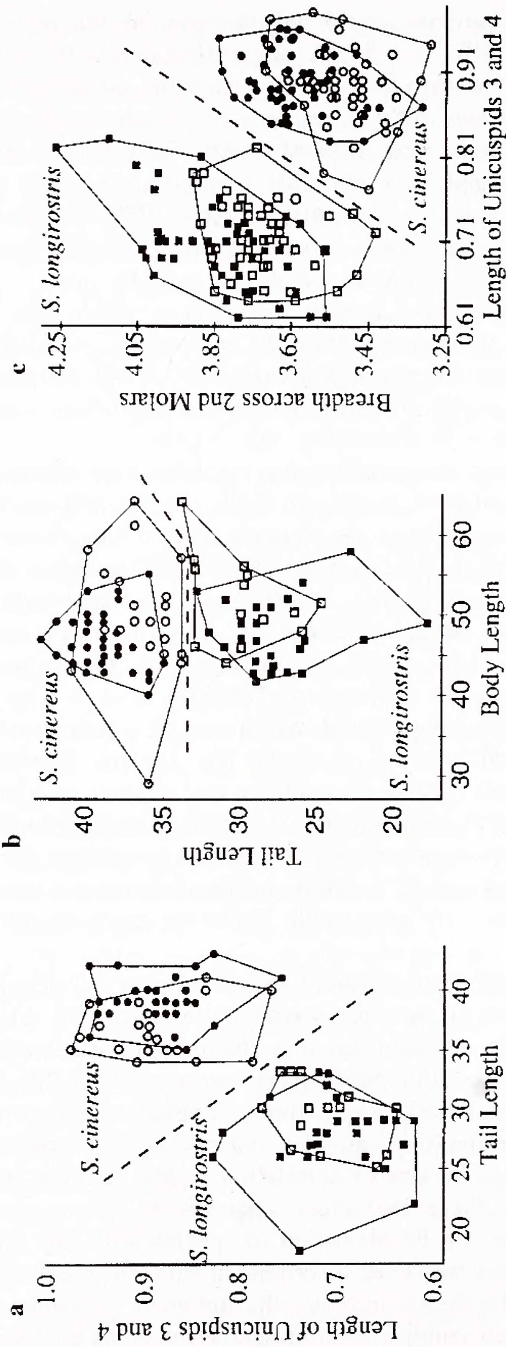


Figure 1. Bivariate scattergrams of raw measurement data from *Sorex longirostris* and *S. cinereus* specimens collected in southern locations (Georgia, North Carolina, South Carolina; filled symbols) and northern locations (Virginia; open symbols) using cranial and external (a); external (b); and cranial characters (c). In (c), a single northern *S. cinereus* specimen falls marginally within the range of points for northern *S. longirostris*.



(1.58, 16.90, and -5.49, respectively), sum the three products, and add a constant (-17.25). The resulting value is the specimen's discriminant score. If the score is greater than zero, the specimens in assigned to *S. cinereus*, otherwise it is assigned to *S. longirostris*. The average discriminant score for *S. cinereus* is 3.06, and the average for *S. longirostris* is -3.18.

Discriminant analysis using cranial and external measurements for the two species correctly classified all specimens with two characters, LU34 and tail length, and this bivariate comparison can be used to identify new specimens without transformation (Fig. 1a). Similarly, using only external characters, all specimens can be identified to species with a bivariate comparison of body and tail lengths (Fig. 1b). Using only cranial characters, specimens can be correctly classified with a high degree of probability (99.5%) with a bivariate comparison of LU34 and BM2 (Fig. 1c).

#### VALIDATION

Validation of the model separating the species showed that the results were stable, as 193 of 200 trial runs produced 100% correct classification. The seven trials producing errors had one misclassification each; therefore, of 7,579 individuals classified in the validation process, only seven were classified incorrectly. All errors were the misclassification of *S. cinereus* specimens.

We validated the utility of this model based upon six test specimens of each species from localities not used in developing the model and with a more conventionally available measuring device (i.e., dial calipers and dissecting microscope). The discriminant analysis was sufficiently robust that all specimens were correctly identified.

#### CONCLUSION

*Sorex cinereus* and *S. longirostris* can be distinguished on the basis of any one of three bivariate plots using untransformed data (Fig. 1) or by discriminant analysis. The results of our univariate comparisons are similar to those of French (1980c) and Greer (1989); we observed a high degree of overlap in all but one mensural character (tail length). Possibly, the separation of the two species by cranial characters in our study is a reflection of the finer scale of measurement permitted by computer assisted video imaging. We should note that regional differences in the morphology of both *S. cinereus* and *S. longirostris* might limit the effectiveness of the methods and characters used by us in mensural discrimination of these two species in areas other than the Southeast.

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## APPENDIX—SPECIMENS EXAMINED

For each species and each state, entries include county, location, number of specimens from that location, and when necessary, acronym of the museum housing the specimen (UGAMNH=University of Georgia Museum of Natural History, USNM=National Museum of Natural History, VCU=Virginia Commonwealth University).

*Sorex longirostris*

GEORGIA (all UGAMNH): Clarke Co.: Athens, Baldwin Avenue, University of Georgia campus, 1. Fulton Co.: Long Island Creek at Chattahoochee River, 10. Lumpkin Co.: Dockery Lake, 3.75 miles N Stone Pile Gap on GA 19, 2. Rabun Co.: Ann Gap Road (FS 410), 2 miles W Low Gap Road, 2. Stephens Co.: Lake Russell Wildlife Management Area, 2; Lake Russell Wildlife Management Area, N of junction of FS Roads 62 and 62A, 1; Lake Russell Wildlife Management Area, Dike 5 Creek at FS 87, 1; Davidson Creek, 220 m upstream from Panther Creek, 3. Union Co.: 1.9 miles WSW Suches, 1; 2.3 miles WSW Suches, 1; 2.0 miles W Suches, 3; GA 180, 0.25 miles North of Lake Winfield Scott, 1.

SOUTH CAROLINA (all UGAMNH): Aiken Co.: Savannah River Plant, Bullfrog Pond, 5; Savannah River Plant, F-Bay, 1; Savannah River Plant, Flamingo Bay, 1; Savannah River Plant, Linda Pond, 1; Savannah River Plant, Pickerel Pond, 1; Savannah River Plant, Rainbow Bay, 5; Savannah River Plant, Sun Bay, 1. Oconee Co.: Sumpter National Forest Road 709, 1.1 miles west of Highway 107, 5. Picken Co.: van Clayton Memorial Highway, 0.9 M below summit of Sassafrass Mountain, 1.

VIRGINIA: Amelia Co.: Amelia Court House, 2 (USNM); Burke, near Seward Forest, 1 (USNM); Falls Church, 1 (USNM); Shenandoah National Park Headquarter, 3 (USNM); Triplett, Seward Forest, 2 (USNM). Chesapeake Co.: Dismal Swamp, Lake Drummond, 2 (USNM). Chesterfield Co.: 4 miles N Keswick Farm, 1 (USNM). Culpepper Co.: 10 miles SE Legnum, 1 (USNM). Cumberland Co.: Columbia (Goochland), 30 (VCU). Essex Co.: 3.5 miles SW Center Cross, 2 (USNM). Fairfax Co.: Fort Belvior, Site 104, 1 (USNM); Fort Belvior, Site CA-5, 1 (USNM). Norfolk Co.: Wallacetown, 4.7 miles NNE, near US 17, 1 (USNM).

*Sorex cinereus*

GEORGIA (All UGAMNH): Rabun Co.: Burnt Cabin Branch, 2 miles N Tate City at North Carolina State line, 4; Rabun Bald, 1; Base of Rabun Bald at Beechgun Gap, 0.2 mile up jeep trail from Gap, 2; FS 150, 4.0 miles S. Dillard at Thomas

Creek, 5; FS 150, 3.1 miles E Dillard at Thomas Creek, 3; FS 150, 2.5 miles E Dillard, 1. Towns Co.: Beech Creek at Tulula River, 1; Swallow Creek Management Area, Fork Ridge, 1; FS 79, E of Mossy Creek Branch, N of Tray Mountain Gap, 9; Swallows Creek Management Area, intersection of FS 698 and FS 698A, 4. White Co.: FS 79, 0.4 miles South Tray Mountain Gap, 4.

NORTH CAROLINA (all UGAMNH): Haywood Co.: Shining Rock, 1. Macon Co.: Coweeta Hydrological Laboratory, 4; Coweeta Hydrological Laboratory, Dryman's Fork, 1; Coweeta Hydrological Laboratory, Lick Branch, 1.

SOUTH CAROLINA (all UGAMNH): Oconee Co.: USFWS Fish Hatchery Visitor Center, 3; 1.0 mile up access road to Fish Hatchery, 5.

VIRGINIA: Giles Co.: Mountain Lake, 1 (USNM); Mountain Lake, 1.7 miles ENE Castle Rock, 2 (USNM); Mountain Lake, 1.8 miles NE Cross Trail, 1 (USNM); Mountain Lake, 2.5 miles NW Ashby Flats, 1 (USNM); Mountain Lake, 2.6 miles NW Ashby Bogs, 1 (USNM); Mountain Lake, 2.7 miles NE Warspur Branch, 1 (USNM); Mountain Lake, 2.7 miles NW Ashby Flat, 3 (USNM); Mountain Lake, 2.7 miles NW Ashby Meadow, 3 (USNM); Mountain Lake, 4.3 miles NNE Castle Rock, 3 (USNM); Mountain Lake, 4.5 miles NE Big Mountain, 1 (USNM); Mountain Lake, 4.5 miles NE Big Soft Seep, 1 (USNM); Mountain Lake, 4.5 miles WNW area 4, 1 (USNM); Mountain Lake, 5 miles NE Bob's Field, 1 (USNM); Mountain Lake, Ashby Bogs, 2 (USNM); Mountain Lake, Butt Mountain, Upper Field, 3 (USNM). Highland Co.: Laurel Fork Area, 21 (VCU); Red Oak Knob, 5 (VCU).